

Appl. No. 09/877,933
AMENDMENT FAXED ON JANUARY 20, 2005
REPLY TO OFFICE ACTION OF DECEMBER 2, 2004

PATENT

REMARKS/ARGUMENTS

Claims 1-6 and 8-16 are presently under consideration and stand substantively rejected. Claims 7 and 17-31 were previously canceled. This response amends claims 1 and 14, cancels claim 4, and adds new claims 32 and 33. Support for the amendment to claims 1 and 14 can be found throughout the specification and at least at page 17, line 24 to page 21, line 5. Support for new claims 32 and 33 can be found throughout the specification and at least at page 5, lines 24-25. Reconsideration of the claims is respectfully requested. The paragraph numbering below follows that of the Office Action.

¶3. Rejection Under 35 U.S.C. §112

Claims 1-16 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking written description in that the application allegedly provides written description only for capture reagents comprising antibodies.

For the purposes of expediting prosecution independent claims 1 and 14 have been amended to recite capture reagents comprising an antibody. Claims 2, 3, 5, 6, and 8-13, and claims 15 and 16 depend either directly or indirectly from independent amended claims 1 and 14, respectively and satisfy the written description requirement for the same reasons. Therefore, the written description requirement should be withdrawn.

Applicants note for the record their disagreement with the Examiner's position. According to MPEP 2163.02, to satisfy the written description requirement, an applicant must convey with reasonable clarity to the artisan that the inventor had possession, as of the filing date sought, of the subject matter now claimed. Applicants respectfully submit that the specification at p. 17, lines 25-29 provides written description of capture reagents encompassing any molecule that is capable of specifically binding to PDI meet the written description requirements.

¶4. Rejection Under 35 U.S.C. §102

Claims 14 and 15 were rejected under 35 U.S.C. §102(e) as allegedly anticipated by U.S. Patent No. 5,798,249 to Braxton et al. ["Braxton"]. This rejection is traversed as follows.

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MPEP 2131 establishes that to anticipate a claim, a cited reference must teach every element of the claim.

According to the Action, Braxton describes a novel *human* protein disulfide isomerase (PDI). Yet amended claim 14 recites a protein disulfide isomerase of *Cryptosporidium parvum*, which is not the same as the human PDI described by Braxton. The attached BLAST report shows little sequence identity between the two. Applicants submit that Braxton fails to teach or suggest an antibody which binds to a protein disulfide isomerase of *Cryptosporidium parvum* as presently claimed, and therefore Braxton fails to anticipate amended claim 14.

Claim 15 depends from claim 14, and is therefore allowable as depending from an allowable base claim, as well as for the novel combination of elements it recites. Withdrawal of this rejection is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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NSC:nap
Attachment: BLAST report and sequences
60377226 v1

NCBI BLAST 2 sequences BLAST Entrez ?

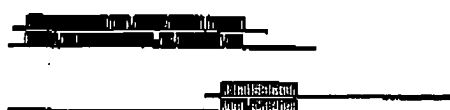
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.2 [Dec-14-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq_1 Length 405 (1..405)

Sequence 2 lc|seq_2 Length 481 (1..481)

Protein Disulfide Isomerase (PDI)



Human
vs.
C. parvum

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 79.0 bits (193), Expect = 6e-14
Identities = 85/351 (24%), Positives = 148/351 (41%), Gaps = 33/351 (9%)

Query: 27 VTTEITSLATENIDEILNADVALVNFYADWCRFSQMLHPFEEASDVKEEFPNENQVV 86
++ ITSL + N ++ + + + +V F+A WC L P F+ I + P V
Sbjct: 31 ISEHITSLTSSNFEDFIKSKEHVIVTFAPWCGHCTALEPEFKATCAEISKLSLSP---PVH 87

Query: 87 FARVDCDQHS DIAQRYRISKYPTLKLFRNGMMKREYRGQRSVKALADYIRQQKSDPIQE 146
VD ++ ++AQ+Y +S YPT+K F +G+ + Y G RS A YI++ +Q
Sbjct: 88 CGSVDATENMELAQGYGVSGYPTIKFP-SGIDSVQNYSGARSKDAFIKYIKKLTGPAVQV 146

Query: 147 IRDLAHTITLDRSKRN-IIG-YEQKDSNRYRVFERNVILHD-DCAFLSAF--GDVSKPE 201
I T+ S + +G+ KDS Y VFE+VA+ + + AF++ F G+
Sbjct: 147 AESEBAIKTIFASSSSAFVGRFTSKDSABYAVFEKVASGCHREHNYAFLAFFQEGEQKLEV 206

Query: 202 RYSGDNIIYKPPGHSAFDMVYLGAMTNFDTYNWIQDKCVPLVREITFEN-GEELTEEG 260
+ + + P + ++ ++ N VPL I+ EN ++ EG
Sbjct: 207 LHKDEEPVSLPMKPTVEELEAKISIMN-----VPLFSAISAENYSLYMSREGY 254

Query: 261 PFLILFHMKEDETESLEIFQNEVARQLISEKGTINFLHADCDKF-RHPLLH--IQKTPA-D 316
E + + + + + F+ D ++F H H I+K P
Sbjct: 255 TANFC---GTNEDFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQHLLIEKFPGLV 310

Query: 317 CPVLAIDSFRHMYVFGDFKDVLIIPGKLKQFVFDLHSGKLHREFPHHGFDPTD 367
+ + S R+MY F V LK+F+ + GK P P +
Sbjct: 311 IQSVNVPSIRYMYGPAKFDSV---EPLKEFMKQVSEGKHELSEIKSEPIPAE 358

Score = 52.8 bits (125), Expect = 5e-06
Identities = 32/121 (26%), Positives = 63/121 (51%), Gaps = 6/121 (4%)

Query: 31 ITSLATENIDEILNADV-ALVNFYADWCRFSQMLHPFEEASDVKEEFPNENQVV 89
+T + + +EI+ +D L+ YA WC + L PI+ + + EE+ + ++VV A+
Sbjct: 363 VTVVVGKTFERIVFRSDKDVLLLEIYAQWCGHCKNLEPTYNQ---LGEEYKDNKDVVIK 418

Query: 90 VDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQSRVKALADYIRQQKSDPIQ-EIR 148
++ Q+ + + +PT+ + G Y G+R+V+A ++I + S P + E R
Sbjct: 419 INGPQNDIPYEGFS PRAFP TILFVKAGTRTPIPYDGKRTVRAFKFISEHSSFPQEKESR 478

Query: 149 D 149
D
Sbjct: 479 D 479

CPU time: 0.05 user secs. 0.00 sys. secs 0.05 total secs.

Gapped

Lambda	K	H
0.321	0.138	0.414

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1380

Number of Sequences: 0

Number of extensions: 121

Number of successful extensions: 6

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 405

length of database: 181,542,687

effective HSP length: 120

effective length of query: 285

effective length of database: 127,752,327

effective search space: 36409413195

effective search space used: 36409413195

T: 9

A: 40

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 71 (32.0 bits)

SEQ ID NO:2 of US Pat. No. 5,798,249 to Braxton et al. (USSN 08/650,275)
Deduced Amino Acid Sequence of Human Protein Disulfide Isomerase (PDI)

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn Ala Asp Val
Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe Ser Gln Met Leu
His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile Lys Glu Glu Phe Pro
Asn Glu Asn Gln Val Val Phe Ala Arg Val Asp Cys Asp Gln His Ser
Asp Ile Ala Gln Arg Tyr Arg Ile Ser Lys Tyr Pro Thr Leu Lys Leu
Phe Arg Asn Gly Met Met Met Lys Arg Glu Tyr Arg Gly Gln Arg Ser
Val Lys Ala Leu Ala Asp Tyr Ile Arg Gln Gln Lys Ser Asp Pro Ile
Gln Glu Ile Arg Asp Leu Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys
Arg Asn Ile Ile Gly Tyr Xaa Glu Gln Lys Asp Ser Asp Asn Tyr Arg
Val Phe Glu Arg Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu
Ser Ala Phe Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn
Ile Ile Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu
Gly Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu Leu
Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys Glu Asp
Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg Gln Leu Ile
Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp Cys Asp Lys Phe
Arg His Pro Leu Leu His Ile Gln Lys Thr Pro Ala Asp Cys Pro Val
Ile Ala Ile Asp Ser Phe Arg His Met Tyr Val Phe Gly Asp Phe Lys
Asp Val Leu Ile Pro Gly Lys Leu Lys Gln Phe Val Phe Asp Leu His
Ser Gly Lys Leu His Arg Glu Phe His His Gly Pro Asp Pro Thr Asp
Thr Ala Pro Gly Glu Gln Ala Gln Asp Val Ala Ser Ser Pro Pro Glu
Ser Ser Phe Gln Lys Leu Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu
Arg Asp Arg Asp Glu Leu

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRF
SQMLHPIFEEASDVKEEFNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMM
KREYRGQRSVKALADYIRQKSDPIQIBIRDLAETTLDRSKRNIGYEQKSDSNYRVFER
VANILHDDCAFLSAFGDVSKPERYSGDNIYKPPGHSAPDMVYLGAMTNFDVTYNWIQ
DKCVPLVREITFENGEBELTEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHAD
CDKFRHPLLHIQKTPADCPVIAIDSFRHMYVFGDFKDVLPGLKQFVFDLHSGKLHREF
HHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

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SEQ ID NO:2 of Instant Application (USSN 09/877,933)

Attorney Docket No. 014907-001910US

Deduced Amino Acid Sequence of *C. parvum* Protein Disulfide Isomerase (PDI)

Met Ile Gly Ile Arg Ser Leu Val Ser Ala Ala Phe Leu Gly Phe Ser
Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser
Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys
Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His
Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser
Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn
Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys
Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser
Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val
Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser
Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr
Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala
Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His
Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu
Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile
Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala
Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile
Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu
Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu
Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg
Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu
Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser
Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly
Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu
Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile
Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile
Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser
Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr
Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe
Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu
Leu

MIGIRSLVSA AFLGFSCLSKVVLGGDEAHFISEHITS LTSSNFEDFIKSKEHVIVTFFAPWC
GHCTALEPEFKATCAEISKLSPPVHCGSV DATENMELAQQYGVSGYPTIKFFSGIDSVQN
YSGARSKDAFIKYIKKLTGPAVQVAESEBAIKTIFASSSSAFVGRFTSKDSA EYAVFEKVA
SGHREHNYAFLIAFFQEGEQKLEVLHKDEE PVSLPMPKTVEELEAKISIMNVPLFSAISAEN
YSLYMSREGYTAWFCGTNEDFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQHLL
IEKFPGLVIQSVNVPSIRYMYGPAKFDSVEPLKEFMKQVSEGKHELSEKSEPIPAEQSGPV
TVVVGKTFEEIVFRSDKDVLL EY AQWCGHCKNLEPIYNQLGEEYKDNDKVVI AKINGP
QNDIPYEGFSPRAFP TILFVKAGTRTPIPYDGKRTVEAFKEFISEHSSFPQEKESRDEL

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